PCT10

ENTERED

RAW SEQUENCE LISTING DATE: 03/19/2003
PATENT APPLICATION: US/10/009,823A TIME: 14:20:51

Input Set : A:\DAVIE150SEQLIST.TXT
Output Set: N:\CRF4\03192003\J009823A.raw

```
 4 <110> APPLICANT: Panaccio, Michael
 5       Rosey, Everett Lee
 6       Sinistaj, Meri
 7       Hasse, Detlef
 8       Parsons, Jim
 9       Ankenbauer, Robert G.
11 <120> TITLE OF INVENTION: LAWSONIA DERIVED GENE AND RELATED FLGE
12       POLYPEPTIDES, PEPTIDES AND PROTEINS AND THEIR USES
15 <130> FILE REFERENCE: DAVI150.001APC
17 <140> CURRENT APPLICATION NUMBER: US 10/009,823A
C--> 18 <141> CURRENT FILING DATE: 2002-08-13
20 <150> PRIOR APPLICATION NUMBER: PCT/AU00/00437
21 <151> PRIOR FILING DATE: 2000-05-11
23 <150> PRIOR APPLICATION NUMBER: US 60/133,973
24 <151> PRIOR FILING DATE: 1999-05-13
26 <160> NUMBER OF SEQ ID NOS: 13
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 502
32 <212> TYPE: PRT
33 <213> ORGANISM: Lawsonia intracellularis
35 <400> SEQUENCE: 1
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37  1               5                  10                  15
38 Thr Gly Leu Gly Thr Val Ser Asn Asn Ile Ala Asn Ala Asn Thr Ile
39             20                  25                  30
40 Gly Tyr Lys Gln Gln Gln Val Val Phe Gln Asp Leu Phe Ser Gln Asp
41         35                  40                  45
42 Leu Ala Ile Gly Ser Thr Gly Ser Gln Gly Pro Asn Gln Ala Gly Met
43     50                  55                  60
44 Gly Ala Gln Val Gly Ser Val Arg Thr Ile Phe Thr Gln Gly Ala Phe
45 65                  70                  75                  80
46 Glu Pro Gly Asn Ser Val Thr Asp Leu Ala Ile Gly Gly Lys Gly Phe
47                 85                  90                  95
48 Phe Gln Val Thr Leu Glu Asp Lys Val His Tyr Thr Arg Ala Gly Asn
49             100                 105                 110
50 Phe Arg Phe Thr Gln Asp Gly Phe Leu Asn Asp Pro Ser Gly Phe Thr
51         115                 120                 125
52 Leu Met Gly Ser Arg Ile Ser Asn Asn Pro Asn Ile Lys Lys Glu Thr
53     130                 135                 140
54 Leu Glu Pro Ile Gln Leu Asp Phe Asn Asp Pro Thr Val Ala Lys Ser
55 145                 150                 155                 160
56 Pro Ala Lys Thr Ser Thr Ala Leu Asn Ala Val Val Asn Leu Gly Asp
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                165                 170                 175
Ser Thr Asp Lys Thr Gln Ser Glu Ala Asn Pro Tyr Phe Ala Leu Leu
            180                 185                 190
Glu Ser Trp Lys Gly Asn Gly Thr Pro Pro Ile Ser Thr Ser Asn Tyr
        195                 200                 205
Ser Tyr Ala Gln Pro Met Arg Val Tyr Asp Gln Gln Gly Asn Ser His
    210                 215                 220
Asp Ile Thr Val Tyr Phe Asp Gly Ala Pro Ser Ser Thr Gly Ser Lys
225                 230                 235                 240
Thr Phe Glu Tyr Leu Val Ala Met Asn Pro Ser Glu Asp Gly Ser Ala
                245                 250                 255
Ala Ser Gly Thr Asp Ser Ala Gly Leu Leu Met Ser Gly Thr Met Thr
            260                 265                 270
Phe Ser Ser Asn Gly Glu Leu Lys Asn Met Thr Ala Phe Thr Pro Thr
        275                 280                 285
Gly Ser Ala Thr Lys Asp Leu Asn Ala Trp Gln Pro Ala Pro Leu Val
    290                 295                 300
Asn Gly Leu Pro Gln Phe Ser Ala Asn Phe Val Gly Ala Gly Ile Gln
305                 310                 315                 320
Pro Leu Thr Leu Asp Phe Gly Ile Lys Ser Gln Gln Asn Met Trp Ala
                325                 330                 335
Gly Ala Pro Ala Ser Ala Ala Ala Ile Gly Thr Asp Ile Gly Lys Leu
            340                 345                 350
Pro Ser Met Met Pro Ile Gln Thr Ser Ser Gly Asn Ser Thr Ala Arg
        355                 360                 365
Asn Gly Ser Ser Ser Thr Arg Arg Tyr Ser Gln Asp Gly Tyr Pro Gln
    370                 375                 380
Gly Asp Leu Val Asp Val Thr Ile Thr Ser Glu Gly Lys Leu Gln Gly
385                 390                 395                 400
Lys Tyr Ser Asn Ser Gln Val Val Asp Phe Tyr Asn Ile Pro Leu Ala
                405                 410                 415
Arg Phe Thr Ser Glu Asp Gly Leu Arg Arg Glu Gly Asn Asn His Tyr
            420                 425                 430
Ser Ala Thr Leu Asp Ser Gly Gly Pro Glu Phe Gly Leu Pro Gly Thr
        435                 440                 445
Ser Asn Tyr Gly Lys Leu Ser Val Asn Gln Leu Glu Thr Ser Asn Val
    450                 455                 460
Asp Met Ser Arg Glu Met Val Asn Met Ile Ile Ile Gln Arg Gly Phe
465                 470                 475                 480
Gln Met Asn Ser Lys Ser Val Thr Thr Ala Asp Thr Met Leu Gln Lys
                485                 490                 495
Ala Leu Glu Leu Lys Arg
            500
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<210> SEQ ID NO: 2
<211> LENGTH: 1509
<212> TYPE: DNA
<213> ORGANISM: Lawsonia intracellularis
<400> SEQUENCE: 2
atgatgggga gtttgtttat tggtgcaaca ggtatgaaaa cccatagtac agggttgggt 60

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    110 tttcaagacc tgtttagtca agatttagca ataggttcta ctggaagtca ggggccaaac 180
    111 caggctggta tgggagcaca ggttggaagt gttcgcacaa tttttacaca gggtgctttt 240
    112 gaacctggca atagtgtaac agatcttgct attggtggaa aaggtttttt tcaggttaca 300
    113 ttagaggata aagtacacta tacacgagca gggaattttc gttttactca agatggtttt 360
    114 ttaaatgatc ctagcggatt tactttaatg ggctcaagaa tatctaataa tcctaacata 420
    115 aaaaaggaaa cccttgaacc aattcagtta gactttaatg atcctacagt agcaaagtct 480
    116 cctgcaaaaa caagtacagc attaaacgct gtggtaaacc ttggtgatag tacagataaa 540
    117 acacaaagtg aagctaatcc atactttgca cttcttgaga gctggaaagg aaatggaaca 600
    118 cctcctattt ctacatcaaa ctactcatat gcacaaccta tgagagtata tgatcaacaa 660
    119 ggaaattctc acgatataac tgtatatttt gatggagcac cctcttcaac aggaagtaaa 720
    120 acatttgaat accttgtagc tatgaatcct agtgaagatg gaagtgctgc atcaggaaca 780
    121 gatagtgcag gtctcttaat gtctggaact atgacatttt caagtaatgg cgaattaaaa 840
    122 aatatgacag cttttactcc tactggctct gcaacaaaag atttaaatgc atggcaacca 900
    123 gcaccattag tcaatggttt accacagttt tcagcaaatt ttgttggtgc aggaatacag 960
    124 cctttaacat tagactttgg aattaaaagc caacagaata tgtgggcagg agctccagca 1020
    125 tccgctgctg ccataggtac agatattggg aaattgccat caatgatgcc aatacaaaca 1080
    126 tccagcggta attctacagc aagaaatgga tcatcttcaa caagaagata tagccaagat 1140
    127 ggttatcctc agggagatct agtagatgtc acaattacct ctgaagggaa attacaaggt 1200
    128 aagtatagta atagtcaggt tgttgatttt tataatattc ctttagcacg ctttacaagt 1260
    129 gaggatggat taagacgaga agggaataac cattattccg caacacttga ctcaggtggg 1320
    130 ccagagtttg gattgccagg aacatctaac tatggaaaac ttagtgtgaa tcaacttgag 1380
    131 acttctaacg tagacatgag cagagaaatg gttaatatga ttattattca acgtggtttt 1440
    132 cagatgaata gtaaatctgt tacaacagca gacacaatgc tacaaaaagc acttgaacta 1500
    133 aagcgttaa                                                        1509
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    136 <211> LENGTH: 21
    137 <212> TYPE: DNA
    138 <213> ORGANISM: Artificial Sequence
    140 <220> FEATURE:
    141 <223> OTHER INFORMATION: Oligonucleotide primer, RA170.
    143 <400> SEQUENCE: 3
    144 ctatttttag gagatgttat c                                          21
    146 <210> SEQ ID NO: 4
    147 <211> LENGTH: 22
    148 <212> TYPE: DNA
    149 <213> ORGANISM: Artificial Sequence
    151 <220> FEATURE:
    152 <223> OTHER INFORMATION: Oligonucleotide primer, RA171.
    154 <400> SEQUENCE: 4
    155 tacaaaatta acaataaaat ac                                         22
    157 <210> SEQ ID NO: 5
    158 <211> LENGTH: 38
    159 <212> TYPE: DNA
    160 <213> ORGANISM: Artificial Sequence
    162 <220> FEATURE:
    163 <223> OTHER INFORMATION: Oligonucleotide primer, FlaF.
W--> 165 <221> NAME/KEY: misc_feature
    166 <222> LOCATION: (1)...(38)
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Input Set : A:\DAVIE150SEQLIST.TXT
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```
     167 <223> OTHER INFORMATION: n = A,T,C or G
W--> 169 <400> 5
W--> 170 gcgaattcca tatgatgggg agtttgttta ttgntgcc                      38
     172 <210> SEQ ID NO: 6
     173 <211> LENGTH: 40
     174 <212> TYPE: DNA
     175 <213> ORGANISM: Artificial Sequence
     177 <220> FEATURE:
     178 <223> OTHER INFORMATION: Oligonucleotide primer, FlgE3'.
     180 <400> SEQUENCE: 6
     181 gctctagaga ctagtcatat taacgcttta gttcaagtgc                      40
     183 <210> SEQ ID NO: 7
     184 <211> LENGTH: 477
     185 <212> TYPE: PRT
     186 <213> ORGANISM: Treponema phagedenis
     188 <400> SEQUENCE: 7
     189 Met Met Arg Ser Leu Phe Ser Gly Val Ser Gly Met Gln Asn His Gln
     190  1               5                  10                  15
     191 Gly Val Asn Pro Lys Glu Val Gly Leu Gly Val Met Val Ala Ser Gly
     192             20                  25                  30
     193 Val Asn Pro Lys Glu Val Gly Leu Gly Val Met Val Ala Ser Thr Arg
     194         35                  40                  45
     195 Met Asp Val Ile Gly Asn Asn Val Ala Asn Val Asn Thr Thr Gly Phe
     196     50                  55                  60
     197 Lys Arg Gly Arg Ile Asp Thr Val His Thr Gln Gly Ala Leu Gln Thr
     198 65                  70                  75                  80
     199 Thr Gly Ile Asn Thr Asp Ile Ala Ile Val Asn Phe Gln Asp Leu Ile
     200                 85                  90                  95
     201 Ser Gln Gln Leu Ser Gly Ala Ser Arg Pro Asn Glu Glu Val Gly Gln
     202             100                 105                 110
     203 Gly Asn Gly Phe Phe Ile Leu Lys Asp Gly Glu Lys Ser Phe Tyr Thr
     204         115                 120                 125
     205 Thr Ala Gly Ala Phe Gly Val Asp Arg Asp Gly Thr Leu Val Asn Pro
     206     130                 135                 140
     207 Ala Asn Gly Ala Cys Asn Leu Asp Lys Arg Leu Met Arg Val Gln Gly
     208 145                 150                 155                 160
     209 Trp Met Ala Glu Asp Ile Glu Gly Gln Gln Ile Ile Asn Thr Ser Asp
     210                 165                 170                 175
     211 Gln Pro Glu Leu Pro Glu Gly Ala Asn Gln Ala Asp Ile Leu Arg Ser
     212             180                 185                 190
     213 Thr Glu Asp Leu Ile Ile Pro Ile Gly Gln Lys Ile Asp Ala Lys Ala
     214         195                 200                 205
     215 Thr Thr Asp Val Ala Tyr Thr Trp Ala Thr Asp Phe Asn Val Tyr Asp
     216     210                 215                 220
     217 Thr Phe Gly Glu Gln His Lys Leu Gln Met Val Phe Ser Arg Val Pro
     218 225                 230                 235                 240
     219 Gly Thr Asn Asn Gln Trp Leu Ala Thr Val Val Thr Asp Thr Ala Gly
     220                 245                 250                 255
     221 Asn Val Thr Ala Pro Asn Val Asp Pro Glu Asn Gln Ala Gly Thr Glu
```

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```
222             260                 265                 270
223 Thr Arg Val Gly Ile Gly Thr Thr Asp Gly Ala Gly Gln Val Leu Val
224         275                 280                 285
225 Gln Ala Thr Glu Asn Thr Phe Ile Val Ser Phe Asp Asn Tyr Gly His
226     290                 295                 300
227 Leu Ala Ser Ser Tyr Asn Val Val Gly Ala Asn Pro Asp Glu Gly Gly
228 305                 310                 315                 320
229 Ala Pro Thr Arg His Thr Phe Asn Ile Asn Asp Gln Ser Gly Ile Ile
230                 325                 330                 335
231 Thr Gly Val Tyr Ser Asn Gly Ala Ser Leu Glu Gly Glu Ile Gly Thr
232             340                 345                 350
233 Ser Arg Asn Thr Ile Thr Gln Phe Ala Glu Arg Glu Ile Gly Gln Leu
234         355                 360                 365
235 Ala Leu Ala Gly Phe Ala Asn Gln Gly Gly Leu Glu Lys Ala Gly Glu
236     370                 375                 380
237 Ser Thr Thr Lys Ala Tyr Gln Gln Asp Gly Tyr Ala Met Gly Tyr Leu
238 385                 390                 395                 400
239 Glu Asn Phe Lys Ile Thr Tyr Ile Gln Ser Asn Asn Ser Gly Ile Ala
240                 405                 410                 415
241 Asn Ile Thr Val Ser Gly Val Met Gly Lys Gly Lys Leu Ile Ala Gly
242             420                 425                 430
243 Thr Leu Glu Met Ser Asn Val Asp Leu Thr Asp Gln Phe Thr Asp Met
244         435                 440                 445
245 Ile Ile Thr Gln Arg Gly Phe Gln Ala Gly Ala Lys Thr Ile Gln Thr
246     450                 455                 460
247 Ser Asp Thr Met Leu Glu Thr Val Leu Asn Leu Lys Arg
248 465                 470                 475
251 <210> SEQ ID NO: 8
252 <211> LENGTH: 462
253 <212> TYPE: PRT
254 <213> ORGANISM: Treponema pallidum
256 <400> SEQUENCE: 8
257 Met Met Arg Ser Leu Phe Ser Gly Val Ser Gly Met Gln Asn His Gln
258  1               5                  10                  15
259 Gly Val Asn Pro Lys Glu Val Gly Leu Gly Val Leu Ile Ala Ser Thr
260             20                  25                  30
261 Arg Met Asp Val Ile Gly Asn Asn Val Ala Asn Val Asn Thr Thr Gly
262         35                  40                  45
263 Phe Lys Arg Gly Arg Ile Asp Thr Val His Thr Gln Gly Ala Leu Gln
264     50                  55                  60
265 Thr Thr Gly Ile Asn Thr Asp Val Ser Ile Val Asn Phe Gln Asp Leu
266 65                  70                  75                  80
267 Ile Ser Gln Gln Leu Ser Ala Ala Ala Arg Pro Asn Glu Glu Val Gly
268                 85                  90                  95
269 Gln Gly Ser Gly Phe Phe Val Leu Lys Ser Gly Glu Lys Thr Phe Phe
270             100                 105                 110
271 Thr Arg Ala Gly Ala Phe Gly Val Asp Asn Ala Gly Thr Leu Val Asn
272         115                 120                 125
273 Pro Ala Asn Gly Ala Cys Asn Leu Asp Lys Arg Leu Met Arg Val Gln
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/19/2003
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 34
Seq#:10; Xaa Pos. 197

VERIFICATION SUMMARY
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L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:165 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:169 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:192